

# Wei Zhao

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

60  
papers

9,511  
citations

31  
h-index

66  
g-index

66  
ext. papers

12,251  
ext. citations

16.4  
avg, IF

3.77  
L-index

#	Paper	IF	Citations
60	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. <i>Molecular Psychiatry</i> , <b>2021</b> , 26, 2111-2125	15.1	3
59	Association of low-frequency and rare coding variants with information processing speed. <i>Translational Psychiatry</i> , <b>2021</b> , 11, 613	8.6	0
58	Genomic profiling of human vascular cells identifies TWIST1 as a causal gene for common vascular diseases. <i>PLoS Genetics</i> , <b>2020</b> , 16, e1008538	6	20
57	Genome-wide association study of cognitive function in diverse Hispanics/Latinos: results from the Hispanic Community Health Study/Study of Latinos. <i>Translational Psychiatry</i> , <b>2020</b> , 10, 245	8.6	1
56	A multi-ancestry genome-wide study incorporating gene-smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. <i>Human Molecular Genetics</i> , <b>2019</b> , 28, 2615-2633	5.6	14
55	Elevated Plasma Ceramides Are Associated With Antiretroviral Therapy Use and Progression of Carotid Artery Atherosclerosis in HIV Infection. <i>Circulation</i> , <b>2019</b> , 139, 2003-2011	16.7	21
54	Combined linkage and association analysis identifies rare and low frequency variants for blood pressure at 1q31. <i>European Journal of Human Genetics</i> , <b>2019</b> , 27, 269-277	5.3	3
53	Genome-wide analysis yields new loci associating with aortic valve stenosis. <i>Nature Communications</i> , <b>2018</b> , 9, 987	17.4	56
52	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. <i>Nature Genetics</i> , <b>2018</b> , 50, 559-571	36.3	221
51	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. <i>American Journal of Human Genetics</i> , <b>2018</b> , 102, 375-400	11	59
50	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. <i>PLoS ONE</i> , <b>2018</b> , 13, e0198166	3.7	31
49	Anxiety and depression in spasmodic dysphonia patients. <i>World Journal of Otorhinolaryngology - Head and Neck Surgery</i> , <b>2018</b> , 4, 110-116	2.6	4
48	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , <b>2018</b> , 50, 26-41	36.3	186
47	Multiplexed Targeted Resequencing Identifies Coding and Regulatory Variation Underlying Phenotypic Extremes of High-Density Lipoprotein Cholesterol in Humans. <i>Circulation Genomic and Precision Medicine</i> , <b>2018</b> , 11, e002070	5.2	5
46	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , <b>2017</b> , 542, 186-190	50.4	412
45	Apolipoprotein(a) isoform size, lipoprotein(a) concentration, and coronary artery disease: a mendelian randomisation analysis. <i>Lancet Diabetes and Endocrinology</i> , <b>2017</b> , 5, 524-533	18.1	111
44	Human knockouts and phenotypic analysis in a cohort with a high rate of consanguinity. <i>Nature</i> , <b>2017</b> , 544, 235-239	50.4	208

43	Loss of Cardioprotective Effects at the Locus as a Result of Gene-Smoking Interactions. <i>Circulation</i> , <b>2017</b> , 135, 2336-2353	16.7	36
42	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. <i>Nature Genetics</i> , <b>2017</b> , 49, 1113-1119	36.3	184
41	and Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. <i>Journal of the American Society of Nephrology: JASN</i> , <b>2017</b> , 28, 981-994	12.7	30
40	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , <b>2017</b> , 49, 1758-1766	36.3	310
39	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. <i>Nature Communications</i> , <b>2017</b> , 8, 910	17.4	78
38	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. <i>American Journal of Human Genetics</i> , <b>2017</b> , 101, 888-902	11	83
37	Systolic Blood Pressure and Risk of Type 2 Diabetes: A Mendelian Randomization Study. <i>Diabetes</i> , <b>2017</b> , 66, 543-550	0.9	22
36	Gene-by-Psychosocial Factor Interactions Influence Diastolic Blood Pressure in European and African Ancestry Populations: Meta-Analysis of Four Cohort Studies. <i>International Journal of Environmental Research and Public Health</i> , <b>2017</b> , 14,	4.6	3
35	Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1006728	6	58
34	Identification of new susceptibility loci for type 2 diabetes and shared etiological pathways with coronary heart disease. <i>Nature Genetics</i> , <b>2017</b> , 49, 1450-1457	36.3	136
33	A novel interaction between the FLJ33534 locus and smoking in obesity: a genome-wide study of 14 131 Pakistani adults. <i>International Journal of Obesity</i> , <b>2016</b> , 40, 186-90	5.5	13
32	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. <i>Nature Genetics</i> , <b>2016</b> , 48, 1151-1161	36.3	181
31	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. <i>Nature Genetics</i> , <b>2016</b> , 48, 1162-70	36.3	152
30	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. <i>Nature Genetics</i> , <b>2016</b> , 48, 1171-1184	36.3	251
29	Using Mendelian Randomization studies to Assess Causality and Identify New Therapeutic Targets in Cardiovascular Medicine. <i>Current Genetic Medicine Reports</i> , <b>2016</b> , 4, 207-212	2.2	4
28	Genome-wide interrogation reveals hundreds of long intergenic noncoding RNAs that associate with cardiometabolic traits. <i>Human Molecular Genetics</i> , <b>2016</b> , 25, 3125-3141	5.6	25
27	Otolaryngology Needs in a Free Clinic Providing Indigent Care. <i>Laryngoscope</i> , <b>2016</b> , 126, 1321-6	3.6	1
26	Genome-Wide Association Analysis of Young-Onset Stroke Identifies a Locus on Chromosome 10q25 Near HABP2. <i>Stroke</i> , <b>2016</b> , 47, 307-16	6.7	39

25	Genome-wide association studies in the Japanese population identify seven novel loci for type 2 diabetes. <i>Nature Communications</i> , <b>2016</b> , 7, 10531	17.4	99
24	Causal Assessment of Serum Urate Levels in Cardiometabolic Diseases Through a Mendelian Randomization Study. <i>Journal of the American College of Cardiology</i> , <b>2016</b> , 67, 407-416	15.1	101
23	Genetic association of long-chain acyl-CoA synthetase 1 variants with fasting glucose, diabetes, and subclinical atherosclerosis. <i>Journal of Lipid Research</i> , <b>2016</b> , 57, 433-42	6.3	14
22	The genetic architecture of type 2 diabetes. <i>Nature</i> , <b>2016</b> , 536, 41-47	50.4	704
21	A replication study of 49 Type 2 diabetes risk variants in a Punjabi Pakistani population. <i>Diabetic Medicine</i> , <b>2016</b> , 33, 1112-7	3.5	3
20	Common and Rare Genetic Variation in CCR2, CCR5, or CX3CR1 and Risk of Atherosclerotic Coronary Heart Disease and Glucometabolic Traits. <i>Circulation: Cardiovascular Genetics</i> , <b>2016</b> , 9, 250-8		14
19	Loss of Function of GALNT2 Lowers High-Density Lipoproteins in Humans, Nonhuman Primates, and Rodents. <i>Cell Metabolism</i> , <b>2016</b> , 24, 234-45	24.6	78
18	A comprehensive 1,000 Genomes-based genome-wide association meta-analysis of coronary artery disease. <i>Nature Genetics</i> , <b>2015</b> , 47, 1121-1130	36.3	1290
17	Physical activity, smoking, and genetic predisposition to obesity in people from Pakistan: the PROMIS study. <i>BMC Medical Genetics</i> , <b>2015</b> , 16, 114	2.1	21
16	Association of HDL cholesterol efflux capacity with incident coronary heart disease events: a prospective case-control study. <i>Lancet Diabetes and Endocrinology</i> , <b>2015</b> , 3, 507-13	18.1	300
15	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , <b>2015</b> , 518, 197-206	50.4	2687
14	Epidemiology and public health policy of tobacco use and cardiovascular disorders in low- and middle-income countries. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , <b>2014</b> , 34, 1811-9	9.4	15
13	Meta-analysis of genome-wide association studies in African Americans provides insights into the genetic architecture of type 2 diabetes. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004517	6	151
12	A novel MMP12 locus is associated with large artery atherosclerotic stroke using a genome-wide age-at-onset informed approach. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004469	6	63
11	Characterizing the empirical distribution of prokaryotic genome n-mers in the presence of nullomers. <i>Journal of Computational Biology</i> , <b>2014</b> , 21, 732-40	1.7	
10	Genome-wide association analysis of blood-pressure traits in African-ancestry individuals reveals common associated genes in African and non-African populations. <i>American Journal of Human Genetics</i> , <b>2013</b> , 93, 545-54	11	145
9	A meta-analysis identifies new loci associated with body mass index in individuals of African ancestry. <i>Nature Genetics</i> , <b>2013</b> , 45, 690-6	36.3	192
8	Support vector machines classifiers of physical activities in preschoolers. <i>Physiological Reports</i> , <b>2013</b> , 1, e00006	2.6	12

7	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. <i>Nature Genetics</i> , <b>2012</b> , 44, 991-1005	36.3	621
6	A simple and sensitive HPLC method for quantification of the metabolin of meclofenoxate in human plasma. <i>Journal of Chromatographic Science</i> , <b>2010</b> , 48, 353-7	1.4	6
5	Human knockouts in a cohort with a high rate of consanguinity		8
4	Rare Non-coding Variation Identified by Large Scale Whole Genome Sequencing Reveals Unexplained Heritability of Type 2 Diabetes		2
3	Scalable generalized linear mixed model for region-based association tests in large biobanks and cohorts		7
2	Tissue-Specific Alteration of Metabolic Pathways Influences Glycemic Regulation		4
1	Discovery and systematic characterization of risk variants and genes for coronary artery disease in over a million participants		5